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FastDB - Fast Pairwise Comparison of Sequences  
 Release 5.4

Results file us-10-071-879-9-inv.res made by jdelaval on Wed 1 Dec 104 15:41:41-PST.

Query sequence being compared: US-10-071-879-9' (1-1908)  
 Number of sequences searched: 1  
 Number of scores above cutoff: 1

Results of the initial comparison of US-10-071-879-9' (1-1908) with:  
 File : ac018798.seq

100-  
 N -  
 U -  
 M -  
 B -  
 E -  
 R -  
 O -  
 F 10-  
 S -  
 E 5-  
 Q -  
 U -  
 U -  
 E -  
 N -  
 C -  
 E -  
 S 0-  
 SCORE 0 128 255 383 511 638 766 894 1021 1149  
 STDEV

1 NUERS E  
 comp.

## PARAMETERS

Similarity matrix Unitary K-tuple 4  
 Mismatch penalty 1 Joining penalty 30  
 Gap penalty 1.00 Window size 32  
 Gap size penalty 0.33  
 Cutoff score 0  
 Randomization group 0

## SEARCH STATISTICS

Scores: Mean Median Standard Deviation  
 1149 0 0.00  
 Times: CPU Total Elapsed  
 00:00:00.95 00:00:01.00  
 Number of residues: 180153  
 Number of sequences searched: 1  
 Number of scores above cutoff: 1

The scores below are sorted by initial score.  
 Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Sig. Frame
1. ac018798	TOIG of: ac018798	check: 176	180153	1149 1597 0.00 0
1. US-10-071-879-9' (1-1908)	TOIG of: ac018798	check: 1761	from: 1 to: 18015	
TOIG of: ac018798	check: 1761	from: 1 to: 180153		
LOCUS	AC018798	180153 bp	DNA	linear HTG 17-AUG-2000
DEFINITION	Homo sapiens chromosome 11 clone RP11-151x8, WORKING DRAFT SEQUENCE, 22 unordered pieces.			
ACCESSION	AC018798			
VERSION	AC018798.7	GI:9838037		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1 (bases 1 to 180153)			
TITLE	Waterston, R.H.			
JOURNAL	The sequence of Homo sapiens clone 2 (bases 1 to 180153)			
REFERENCE	Waterston, R.H.			
AUTHORS	2 (bases 1 to 180153)			
TITLE	Unpublished			
JOURNAL	Submitted (19-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA			
COMMENT	On Aug 17, 2000 this sequence version replaced gi:8567925.			

## Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

Project information

Center project name: H NH0015108

Summary Statistics

Sequencing vector: M13, 864

Sequencing vector: plasmid, 144

Chemistry: Dye-terminator Big Dye, 144 of reads

Chemistry: Dye-terminator Big Dye, 144 of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 169308 bases at least Q40

Consensus quality: 174059 bases at least Q30

Insert size: 171000; agarose-fp

Insert size: 179077; sum-of-contigs

Quality coverage: 4.43 in Q20 bases; agarose-fp

Quality coverage: 4.28 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1756: contig of 1756 bp in length  
 1757 1856: gap of unknown length  
 1857 3442: contig of 1586 bp in length  
 3443 3543: gap of unknown length  
 3543 6427: contig of 2885 bp in length  
 6427 6428: gap of unknown length  
 6428 9099: contig of 2472 bp in length  
 9099 9000: gap of unknown length  
 9000 10529: contig of 1430 bp in length  
 10529 10530: gap of unknown length  
 10530 14118: contig of 3489 bp in length  
 14118 14119: gap of unknown length



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 570 580 590 600 610 620 630  
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O | O Intell:Genetics  
> O <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-10-071-879-9.res made by jdelaval on Wed 1 Dec 104 15:40:25-EST.

Query sequence being compared: US-10-071-879-9 (1-1908)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-10-071-879-9 (1-1908) with:  
File : ac018798.seq

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100-
N -
U - 50-
M -
B -
E -
R -
O -
F - 10-
S -
E - 5-
U -
O -
N -
C -
E -
S - 0-
SCORE 0 15 30 44 59 74 89 103 118 133
STDDEV

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## PARAMETERS

Similarity matrix                    Unitary                    K-tuple  
Mismatch penalty                    1                    Joining penalty  
Gap penalty                    1.00                    Window size  
Gap size penalty                    0.33  
Cutoff score                    0  
Randomization group                    0

## SEARCH STATISTICS

Scores:                    Mean                    Median                    Standard Deviation  
                             133                    0                    0.00  
Times:                    CPU                    Total Elapsed  
                             00:00:00.05                    00:00:01.00

Number of residues:                    180153  
Number of sequences searched:                    1  
Number of scores above cutoff:                    1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Score	Init. Opt.	Sig. Frame
---------------	-------------	--------	-------	-------	------------	------------

1. ac018798	TOIG of: ac018798	check: 176	180153	133	763	0.00 0
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1. US-10-071-879-9 (1-1908)  
ac018798                    TOIG of: ac018798                    check: 1761                    from: 1                    to: 18015

TOIG of: ac018798                    check: 1761                    from: 1                    to: 180153

LOCUS                    AC018798                    180153 bp                    DNA                    linear                    HTG 17-AUG-2000  
DEFINITION                    Homo sapiens chromosome 11 clone RP11-15L8, WORKING DRAFT SEQUENCE,  
22 unordered pieces.  
ACCESSION                    AC018798  
VERSION                    AC018798.7                    GI:9838037  
KEYWORDS                    HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE                    Homo sapiens (human)  
ORGANISM                    Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 180153)  
Waterston,R.H.  
The sequence of Homo sapiens clone  
Unpublished  
2 (bases 1 to 180153)  
Waterston,R.H.  
Submitted (19-DEC-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Aug 17, 2000 this sequence version replaced gi:8567925.

## Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Project information

Center project name: H.NH0015108

Summary Statistics

Sequencing vector: M13; 864

Sequencing vector: plasmid; 144

Chemistry: Dye-terminator Big Dye; 144 of reads

Chemistry: Dye-terminator Big Dye; 144 of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 169308 bases at least Q40

Consensus quality: 174059 bases at least Q30

Insert size: 171000; agarose-fp

Insert size: 179077; sum-of-contigs

Quality coverage: 4.43 in Q20 bases; agarose-fp

Quality coverage: 4.28 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 22 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1  
\* 1757                    1756: contig of 1756 bp in length  
\* 1857                    1856: gap of unknown length  
\* 3442                    3442: contig of 1586 bp in length  
\* 3443                    3442: gap of unknown length  
\* 6427                    6427: contig of 2885 bp in length  
\* 6428                    6427: gap of unknown length  
\* 6528                    6528: contig of 2472 bp in length  
\* 9099                    9099: gap of unknown length  
\* 9100                    9100: gap of unknown length  
\* 10629                    10629: contig of 1430 bp in length  
\* 10630                    10629: gap of unknown length  
\* 14118                    14118: contig of 3489 bp in length  
\* 14119                    14218: gap of unknown length





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